Step 1 – Load the data:

In [1]:
```
# Import Packages
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
%matplotlib inline
```

In [19]:
```
columns = ['Sepal length', 'Sepal width', 'Petal length', 'Petal width', 'Class_labels']
# Load the data
df = pd.read_csv('iris.data', names=columns)
df.head()
```

Out[19]:

	Sepal length	Sepal width	Petal length	Petal width	Class_labels
0	5.1	3.5	1.4	0.2	Iris-setosa
1	4.9	3.0	1.4	0.2	Iris-setosa
2	4.7	3.2	1.3	0.2	Iris-setosa
3	4.6	3.1	1.5	0.2	Iris-setosa
4	5.0	3.6	1.4	0.2	Iris-setosa

Step 2 – Analyze and visualize the dataset:

In [20]:
```
# Some basic statistical analysis about the data
df.describe()
```

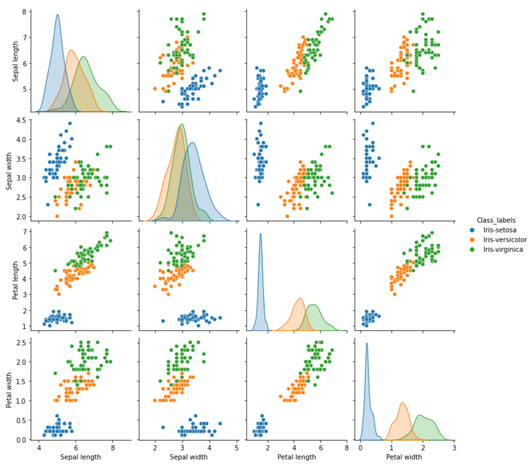
Out[20]:

	Sepal length	Sepal width	Petal length	Petal width
count	150.000000	150.000000	150.000000	150.000000
mean	5.843333	3.054000	3.758667	1.198667
std	0.828066	0.433594	1.764420	0.763161
min	4.300000	2.000000	1.000000	0.100000
25%	5.100000	2.800000	1.600000	0.300000
50%	5.800000	3.000000	4.350000	1.300000
75%	6.400000	3.300000	5.100000	1.800000
max	7.900000	4.400000	6.900000	2.500000

From this description, we can see all the descriptions about the data, like average length and width, minimum value, maximum value, the 25%, 50%, and 75% distribution value, etc.

In [22]:
```
# Visualize the whole dataset
sns.pairplot(df, hue='Class_labels')
```

Out[22]:
```
<seaborn.axisgrid.PairGrid at 0x14f67467b80>
```



1.From this visualization, we can tell that iris-setosa is well separated from the other two flowers.

2.And iris virginica is the longest flower and iris setosa is the shortest.

In [23]:
```
# Separate features and target
data = df.values
X = data[:,0:4]
Y = data[:,4]
```

In [24]:
```
# Calculate average of each features for all classes
Y_Data = np.array([np.average(X[:, i][Y==j].astype('float32')) for i in range (X.shape[1])
 for j in (np.unique(Y))])
Y_Data_reshaped = Y_Data.reshape(4, 3)
Y_Data_reshaped = np.swapaxes(Y_Data_reshaped, 0, 1)
X_axis = np.arange(len(columns)-1)
width = 0.25
```

1.Np.average calculates the average from an array.

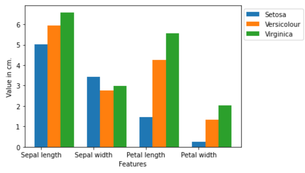
2.Here we used two for loops inside a list. This is known as list comprehension.

3.List comprehension helps to reduce the number of lines of code.

4.The Y_Data is a 1D array, but we have 4 features for every 3 classes. So we reshaped Y_Data to a (4, 3) shaped array.

5.Then we change the axis of the reshaped matrix.

In [25]:
```
# Plot the average
plt.bar(X_axis, Y_Data_reshaped[0], width, label = 'Setosa')
plt.bar(X_axis+width, Y_Data_reshaped[1], width, label = 'Versicolour')
plt.bar(X_axis+width*2, Y_Data_reshaped[2], width, label = 'Virginica')
plt.xticks(X_axis, columns[:4])
plt.xlabel("Features")
plt.ylabel("Value in cm.")
plt.legend(bbox_to_anchor=(1.3,1))
plt.show()
```



1.We used matplotlib to show the averages in a bar plot.

2.Here we can clearly see the verginica is the longest and setosa is the shortest flower.

Step 3 – Model training:

In [26]:
```
# Split the data to train and test dataset.
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, Y, test_size=0.2)
```

1.Using train_test_split we split the whole data into training and testing datasets. Later we'll use the testing dataset to check the accuracy of the model.

In [27]:
```
# Support vector machine algorithm
from sklearn.svm import SVC
svn = SVC()
svn.fit(X_train, y_train)
```

Out[27]:
```
SVC()
```

1.Here we imported a support vector classifier from the scikit-learn support vector machine.

2.Then, we created an object and named it svn.

3.After that, we feed the training dataset into the algorithm by using the svn.fit() method.

Step 4 – Model Evaluation:

In [28]:
```
# Predict from the test dataset
predictions = svn.predict(X_test)
# Calculate the accuracy
from sklearn.metrics import accuracy_score
accuracy_score(y_test, predictions)
```

Out[28]:
```
0.9333333333333333
```

1.Now we predict the classes from the test dataset using our trained model.

2.Then we check the accuracy score of the predicted classes.

3.accuracy_score() takes true values and predicted values and returns the percentage of accuracy.

In [29]:
```
# A detailed classification report
from sklearn.metrics import classification_report
print(classification_report(y_test, predictions))
```

```
                precision    recall  f1-score   support

    Iris-setosa       1.00      1.00      1.00        10
Iris-versicolor       0.83      1.00      0.91        10
 Iris-virginica       1.00      0.80      0.89        10

       accuracy                           0.93        30
      macro avg       0.94      0.93      0.93        30
   weighted avg       0.94      0.93      0.93        30
```

1.The classification report gives a detailed report of the prediction.

2.Precision defines the ratio of true positives to the sum of true positive and false positives.

3.Recall defines the ratio of true positive to the sum of true positive and false negative.

4.F1-score is the mean of precision and recall value.

5.Support is the number of actual occurrences of the class in the specified dataset.

Step 5 – Testing the model:

In [30]:
```
X_new = np.array([[3, 2, 1, 0.2], [  4.9, 2.2, 3.8, 1.1 ], [  5.3, 2.5, 4.6, 1.9 ]])
#Prediction of the species from the input vector
prediction = svn.predict(X_new)
print("Prediction of Species: {}".format(prediction))
```

```
Prediction of Species: ['Iris-setosa' 'Iris-versicolor' 'Iris-versicolor']
```

1.Here we take some random values based on the average plot to see if the model can predict accurately.

In [ ]:
```
```